

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L. et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29,188
 - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

09276796-060704

(2) INFORMATION FOR SEQ. ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(ix) FEATURES:

(D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.8b

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
 (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC	36
Met Lys Leu Leu	
-15	
TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG	81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu	
-10 -5 1	
ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT	126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys	
5 10 15	
CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC	171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg	
20 25 30	
AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT	216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe	
35 40 45	
TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG	261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val	
50 55 60	
GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC	306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn	
65 70 75	
GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA	351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg	
80 85 90	
GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG	396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met	
95 100 105	
AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA	439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *	
110 115	
CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAT AAAGTGTTTC	489
TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG	539
CGGCCGCGGG CCCATCGTTT TCCACCC	566

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
 -15 -10 -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
 1 5 10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala
 15 20 25 30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
 35 40 45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
 50 55 60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu
 65 70 75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val
 80 85 90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro
 95 100 105 110

Lys Phe Ser Pro Val Asp *
 115

09676756-060701

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

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(ix)FEATURES
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(D) OTHER INFORMATION: Mature Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
1 5 10 15

Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
20 25 30

Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
35 40 45

Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp
50 55 60

Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
65 70 75 80

Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
85 90 95

Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
100 105 110

Ser Pro Val Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC	46
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTAATA	455
Ile Asp *	
115	
TCGTTATGTA AAAAAAAAAA AAAAAA	481

(2) INFORMATION FOR SEQ. ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA	455
Ile Asp *	
115	
TCGTTATGAA AAAAAAAAAA AAAAAAA	482

09876796-060701

(2) INFORMATION FOR SEQ. ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1          5          10          15
Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20          25          30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35          40          45
Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50          55          60
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65          70          75          80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85          90          95
Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100        105        110
Pro Ile Asp *
115

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- (2) INFORMATION FOR SEQ. ID NO: 9
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 3.4
 (ix) FEATURES
 (D) OTHER INFORMATION: Non-His-tagged, Signal plus
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 91
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC 136
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG 316
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
 85 90 95

GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406
 Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
 100 105 110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 455
 Ile Asp *
 115

TCGTTATGTA AAAAAAAAAA AAAAAA 481

09876543210 "060704"

(2) INFORMATION FOR SEQ. ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
    1                5                10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15                20                25                30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
    35                40                45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
    50                55                60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
    65                70                75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
    80                85                90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
    95                100                105                110

Phe Ser Pro Ile Asp *
                115

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09030701-060295

(2) INFORMATION FOR SEQ. ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
 1 5 10 15
 Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
 20 25 30
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
 35 40 45
 Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
 50 55 60
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
 65 70 75 80
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
 85 90 95
 Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110
 Pro Ile Asp *
 115

09876796-060701
 102090-967960

(2) INFORMATION FOR SEQ. ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA	455
Ile Asp *	
115	
TCGTTATGAA AAAAAAAAAA AAAAAAA	482

(2) INFORMATION FOR SEQ. ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Mature protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1          5          10          15
Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20          25          30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35          40          45
Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50          55          60
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65          70          75          80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85          90          95
Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100         105         110
Pro Ile Asp *
115

```

09876796-060701

(2) INFORMATION FOR SEQ. ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      90
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC     136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT     181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA     226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC     271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG     316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT     361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT     406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGGCTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```

09876796-060701

(2) INFORMATION FOR SEQ. ID NO: 16

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.2
(ix) FEATURES
 (D) OTHER INFORMATION: His-tagged, Signal plus
```

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  
Met Gly Ser Ser His His His His His His Ser  
-55 -50

96

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-45 -40 -35

141

GGA CAG CAA ATG GGT CGC GGA TTC GAA TTC GCA CGA GCA AAA ATG  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met  
-30 -25 -20

186

AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT  
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

231

CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC  
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser

276

AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC  
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp  
15 20 25

321

AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG  
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys  
30 35 40

366

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC  
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala  
45 50 55

411

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG  
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val

456

GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC  
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val  
75 80 85

501

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT  
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys

546

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA  
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

595

TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA

645

AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT

681

## (2) INFORMATION FOR SEQ. ID NO: 17

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

```

09876796-050701

## (2) INFORMATION FOR SEQ. ID NO: 18

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

## (ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, signal minus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |

## (2) INFORMATION FOR SEQ. ID NO: 19

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

```

- (2) INFORMATION FOR SEQ. ID NO: 20
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 682 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.3
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal Plus

09876756-060701

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

|                                                                |     |
|----------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG         | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC     | 96  |
| Met Gly Ser Ser His His His His His His Ser                    |     |
| -55 -50                                                        |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT    | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly    |     |
| -45 -40 -35                                                    |     |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG    | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met    |     |
| -30 -25 -20                                                    |     |
| AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT    | 231 |
| Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala    |     |
| -15 -10 -5                                                     |     |
| CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC    | 276 |
| Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser    |     |
| 1 5 10                                                         |     |
| AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC    | 321 |
| Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp    |     |
| 15 20 25                                                       |     |
| AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG    | 366 |
| Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys    |     |
| 30 35 40                                                       |     |
| CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC    | 411 |
| His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala    |     |
| 45 50 55                                                       |     |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG    | 456 |
| Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val    |     |
| 60 65 70                                                       |     |
| GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC    | 501 |
| Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val    |     |
| 75 80 85                                                       |     |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT    | 546 |
| Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys    |     |
| 90 95 100                                                      |     |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA | 595 |
| Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *              |     |
| 105 110 115                                                    |     |
| TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA         | 645 |
| AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT                      | 682 |

09876756-060701

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

```
(ix)FEATURES
```

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115



## (2) INFORMATION FOR SEQ. ID NO: 22

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

## (ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal minus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |

(2) INFORMATION FOR SEQ. ID NO: 23

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 149 Amino Acids
    (B) TYPE: Amino Acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Protein
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Tenebrio molitor
    (B) INDIVIDUAL/ISOLATE: none
    (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: cDNA
    (B) CLONE: 2.3
(ix) FEATURES
    (D) OTHER INFORMATION: Mature Protein with
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
```

[illegible]

- (2) INFORMATION FOR SEQ. ID NO: 24
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

0527396-050704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50
 AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96
 Met Gly Ser Ser His His His His His His Ser
 -65 -60 -55
 AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
 Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
 -50 -45 -40
 GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT 186
 Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile
 -35 -30 -25
 CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC 231
 Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser
 -20 -15 -10
 CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT 276
 Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
 -5 1 5
 GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA 321
 Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly
 10 15 20
 GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG 366
 Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu
 25 30 35
 GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC 411
 Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn
 40 45 50
 GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG 456
 Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu
 55 60 65
 AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG 501
 Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu
 70 75 80
 AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG 546
 Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
 85 90 95
 ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG 595
 Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
 100 105 110
 TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG 643
 Phe Ser Pro Val Asp *
 115
 TGTGCTTTAC ATATAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA 693
 AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT 743
 TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT 777

(2) INFORMATION FOR SEQ. ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

```
(iv) ANTI-SENSE: no
```

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
-25 -20 -15 -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
-5 1 5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
10 15 20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
25 30 35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
40 45 50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
55 60 65 70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
75 80 85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
90 95 100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *

- (2) INFORMATION FOR SEQ. ID NO: 26
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -30                               -25                               -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -15                               -10                               -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
   1                               5                               10                               15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
   20                               25                               30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys
   35                               40                               45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val
   50                               55                               60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu
   65                               70                               75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu
   80                               85                               90                               95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
   100                              105                              110

Phe Ser Pro Val Asp *
   115

```

- (2) INFORMATION FOR SEQ. ID NO: 28
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

060701-060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

	TTGTTAGCGG	ATGGAATTCC	CTCGTAGGGG	ATAATTTTGT	TTACTTTAAG		50
AAGGAGATAT	ACC	ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC				96	
		Met Gly Ser Ser His His His His His His Ser	-55		-50		
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT						141	
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	-45		-40		-35		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG						186	
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	-30		-25		-20		
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT						231	
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	-15		-10		-5		
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC						276	
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	1		5		10		
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC						321	
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	15		20		25		
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG						366	
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	30		35		40		
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC						411	
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	45		50		55		
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG						456	
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	60		65		70		
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC						501	
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	75		80		85		
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT						546	
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val	90		95		100		
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA						595	
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	105		110		115		
TTTGACTGAA TTTTGACAAT AAAGGTACTA TC GTTATGTA AAAAAAAAAA						645	
AAAAAACTCG AGCACCAACCA CCACCAACCAC TGAGAT						681	

(2) INFORMATION FOR SEQ. ID NO: 29

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Precursor protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
90 95 100

```
Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
      105                      110                      115
```

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

MOLECULE TYPE: cDNA t

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

```
(iv) ANTI-SENSE: no
```

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96

Met Gly Ser Ser His His His His His His Ser
-30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141

Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186

Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231

Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321

Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366

Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys
55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411

Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile
70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456

Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
85 90 95

TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501

Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543

Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

- (2) INFORMATION FOR SEQ. ID NO: 32
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

05876795-050701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

(2) INFORMATION FOR SEQ. ID NO: 33

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

```
(iv) ANTI-SENSE: no
```

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
55 60 65 70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

- (2) INFORMATION FOR SEQ. ID NO: 34
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 36

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 7.5
(ix) FEATURES
 (D) OTHER INFORMATION: His-tagged, Signal plus
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

|            |            |            |            |            |     |     |     |     |     |     |     |     |            |     |     |
|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|------------|-----|-----|
| TTGTTAGCGG | ATGGAATTCC | CTCGTAGGGG | ATAATTTTGT | TTACTTTAAG | 50  |     |     |     |     |     |     |     |            |     |     |
| AAGGAGATAT | ACC        | ATG        | GGC        | AGC        | AGC | CAT | CAT | CAT | CAT | CAT | CAC | AGC | 96         |     |     |
|            |            | Met        | Gly        | Ser        | Ser | His | His | His | His | His | His | Ser |            |     |     |
|            |            |            |            | -55        |     |     |     |     |     |     |     | -50 |            |     |     |
| AGC        | GGC        | CTG        | GTG        | CCG        | CGC | GGC | AGC | CAT | ATG | GCT | AGC | ATG | ACT        | GGT | 141 |
| Ser        | Gly        | Leu        | Val        | Pro        | Arg | Gly | Ser | His | Met | Ala | Ser | Met | Thr        | Gly |     |
|            | -45        |            |            |            |     | -40 |     |     |     |     | -35 |     |            |     |     |
| GGA        | CAG        | CAA        | ATG        | GGT        | CGC | GGA | TCC | GAA | TTC | GCA | CGA | GCA | AAA        | ATG | 186 |
| Gly        | Gln        | Gln        | Met        | Gly        | Arg | Gly | Ser | Glu | Phe | Ala | Arg | Ala | Lys        | Met |     |
|            | -30        |            |            |            |     | -25 |     |     |     |     | -20 |     |            |     |     |
| AAA        | CTC        | CTC        | TTG        | TGC        | TTT | GCG | TTC | GCC | GCC | ATC | GTC | ATC | GGA        | GCT | 231 |
| Lys        | Leu        | Leu        | Leu        | Cys        | Phe | Ala | Phe | Ala | Ala | Ile | Val | Ile | Gly        | Ala |     |
|            | -15        |            |            |            |     | -10 |     |     |     |     | -5  |     |            |     |     |
| CAG        | GCT        | CTC        | ACC        | GAC        | GAA | CAG | ATA | CAG | AAA | AGG | AAC | AAG | ATC        | AGC | 276 |
| Gln        | Ala        | Leu        | Thr        | Asp        | Glu | Gln | Ile | Gln | Lys | Arg | Asn | Lys | Ile        | Ser |     |
|            | 1          |            |            |            | 5   |     |     |     |     |     | 10  |     |            |     |     |
| AAA        | GAG        | TGC        | CAG        | CAG        | GTG | TCC | GGA | GTG | TCC | CAA | GAG | ACG | ATC        | GAC | 321 |
| Lys        | Glu        | Cys        | Gln        | Gln        | Val | Ser | Gly | Val | Ser | Gln | Glu | Thr | Ile        | Asp |     |
|            | 15         |            |            |            |     | 20  |     |     |     |     | 25  |     |            |     |     |
| AAA        | GTC        | CGC        | ACA        | GGT        | GTC | TTG | GTC | GAC | GAT | CCC | AAA | ATG | AAG        | AAG | 366 |
| Lys        | Val        | Arg        | Thr        | Gly        | Val | Leu | Val | Asp | Asp | Pro | Lys | Met | Lys        | Lys |     |
|            | 30         |            |            |            |     | 35  |     |     |     |     | 40  |     |            |     |     |
| CAC        | GTC        | CTC        | TGC        | TTC        | TCG | AAG | AAA | ACT | GGA | GTG | GCA | ACC | GAA        | GCC | 411 |
| His        | Val        | Leu        | Cys        | Phe        | Ser | Lys | Lys | Thr | Gly | Val | Ala | Thr | Glu        | Ala |     |
|            | 45         |            |            |            |     | 50  |     |     |     |     | 55  |     |            |     |     |
| GGA        | GAC        | ACC        | AAT        | GTG        | GAG | GTA | CTC | AAA | GCC | AAG | CTG | AAG | CAT        | GTG | 456 |
| Gly        | Asp        | Thr        | Asn        | Val        | Glu | Val | Leu | Lys | Ala | Lys | Leu | Lys | His        | Val |     |
|            | 60         |            |            |            |     | 65  |     |     |     |     | 70  |     |            |     |     |
| GCC        | AGC        | GAC        | GAA        | GAG        | GTG | GAC | AAG | ATC | GTG | CAG | AAG | TGC | GTG        | GTC | 501 |
| Ala        | Ser        | Asp        | Glu        | Glu        | Val | Asp | Lys | Ile | Val | Gln | Lys | Cys | Val        | Val |     |
|            | 75         |            |            |            |     | 80  |     |     |     |     | 85  |     |            |     |     |
| AAG        | AAG        | GCC        | ACA        | CCA        | GAG | GAA | ACG | GCT | TAT | GAC | ACC | TTC | AAG        | TGT | 546 |
| Lys        | Lys        | Ala        | Thr        | Pro        | Glu | Glu | Thr | Ala | Tyr | Asp | Thr | Phe | Lys        | Cys |     |
|            | 90         |            |            |            |     | 95  |     |     |     |     | 100 |     |            |     |     |
| ATT        | TAC        | GAC        | AGT        | AAA        | CCT | GAT | TTC | TCT | CCT | ATT | GAT | TAA | TTGTTTTGTA | 595 |     |
| Ile        | Tyr        | Asp        | Ser        | Lys        | Pro | Asp | Phe | Ser | Pro | Ile | Asp | *   |            |     |     |
|            | 105        |            |            |            |     | 110 |     |     |     |     | 115 |     |            |     |     |
| TTTGGCTGAA | TTTGGACAAT | AAAGGTACTA | TCGTTATGTA | AAAAAAAAAA | 645 |     |     |     |     |     |     |     |            |     |     |
| AAAAAACTCG | AGCACCACCA | CCACCACCAC | TGAGAT     | 681        |     |     |     |     |     |     |     |     |            |     |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iv) ANTI-SENSE: no

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

## (2) INFORMATION FOR SEQ. ID NO: 38

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |

## (2) INFORMATION FOR SEQ. ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 40
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-HI site
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG 24

104090-962360

## (2) INFORMATION FOR SEQ. ID NO: 41

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Tenebrio molitor
    (B) INDIVIDUAL/ISOLATE: none
    (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: cDNA
    (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
(ix) FEATURES
    (D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
```

GAGAGGATAA CTAATTGAGC TCGCC 25

(2) INFORMATION FOR SEQ. ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA 24

(2) INFORMATION FOR SEQ. ID NO: 43

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 13.17
(ix) FEATURES
 (D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
```

GAGTGGTCAA CTAAGTGAGC TCGCC 25

## (2) INFORMATION FOR SEQ. ID NO: 44

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
|------------|--------------|--------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GGCACGAGCA | AAA          | ATG    | AAA        | CTC        | CTC        | TTG        | TGC | TTT | GCN | TTC | GCC | GCC |     | 46  |     |
|            |              | Met    | Lys        | Leu        | Leu        | Leu        | Cys | Phe | Ala | Phe | Ala | Ala |     |     |     |
|            |              |        |            |            |            | -15        |     |     |     |     |     |     |     | -10 |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| ATC        | GTC          | ATC    | GGA        | GCT        | CAG        | GCT        | CTC | ACC | GAY | GAA | CAG | ATA | CAG | AAA | 91  |
| Ile        | Val          | Ile    | Gly        | Ala        | Gln        | Ala        | Leu | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|            |              | -5     |            |            |            |            | 1   |     |     |     | 5   |     |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| AGG        | AAC          | AAG    | ATC        | AGC        | AAA        | GAR        | TGC | CAG | CAG | GNG | TCC | GGA | GTG | TCC | 136 |
| Arg        | Asn          | Lys    | Ile        | Ser        | Lys        | Glu        | Cys | Gln | Gln | Val | Ser | Gly | Val | Ser |     |
|            |              | 10     |            |            |            |            | 15  |     |     |     |     | 20  |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| CAA        | GAG          | ACG    | ATC        | GAC        | AAA        | GTC        | CGC | ACA | GGT | GTC | TTG | GTC | GAY | GAT | 181 |
| Gln        | Glu          | Thr    | Ile        | Asp        | Lys        | Val        | Arg | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|            |              | 25     |            |            |            |            | 30  |     |     |     |     | 35  |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| CCC        | AAA          | ATG    | AAG        | AAG        | CAC        | GTC        | CTC | TGC | TTC | TCG | AAG | ARA | ACT | GGA | 226 |
| Pro        | Lys          | Met    | Lys        | Lys        | His        | Val        | Leu | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|            |              | 40     |            |            |            |            | 45  |     |     |     |     | 50  |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| GTG        | GCA          | ACC    | GAA        | GCC        | GGA        | GAC        | ACC | AAT | GTG | GAG | GTA | CTC | AAA | GCC | 271 |
| Val        | Ala          | Thr    | Glu        | Ala        | Gly        | Asp        | Thr | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|            |              | 55     |            |            |            |            | 60  |     |     |     |     | 65  |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| AAG        | CTG          | AAG    | CAT        | GTG        | GCC        | AGC        | GAC | GAA | GAR | GTG | GAC | AAG | ATC | GTG | 316 |
| Lys        | Leu          | Lys    | His        | Val        | Ala        | Ser        | Asp | Glu | Glu | Val | Asp | Lys | Ile | Val |     |
|            |              | 70     |            |            |            |            | 75  |     |     |     |     | 80  |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| CAG        | AAG          | TGC    | GTG        | GTC        | AAG        | AAG        | GCC | ACA | CCA | GAG | GAA | ACG | GCT | TAT | 361 |
| Gln        | Lys          | Cys    | Val        | Val        | Lys        | Lys        | Ala | Thr | Pro | Glu | Glu | Thr | Ala | Tyr |     |
|            |              | 85     |            |            |            |            | 90  |     |     |     |     | 95  |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| GAC        | ACC          | TTC    | AAG        | NNT        | ATT        | TAC        | GAC | AGT | AAA | CCT | GAT | TTC | TCT | CCT | 406 |
| Asp        | Thr          | Phe    | Lys        | Cys        | Ile        | Tyr        | Asp | Ser | Lys | Pro | Asp | Phe | Ser | Pro |     |
|            |              | 100    |            |            |            |            | 105 |     |     |     |     | 110 |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| ATT        | GAT          | TAA    | TTGTTTTGTA | TTTGRCTGAA | TTTTGACAAT | AAAGGTANTA |     |     |     |     |     |     |     |     | 455 |
| Ile        | Asp          | *      |            |            |            |            |     |     |     |     |     |     |     |     |     |
|            |              | 115    |            |            |            |            |     |     |     |     |     |     |     |     |     |
|            |              |        |            |            |            |            |     |     |     |     |     |     |     |     |     |
| TCGTTATGNA | AAAAAAAAAAAA | AAAAAA |            |            |            |            |     |     |     |     |     |     |     |     | 481 |

## (2) INFORMATION FOR SEQ. ID NO: 45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYC NYC RYY 46
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
 -15 -10

NTN NTN RTC RNA GYT CAG GCY CTN ACC GAN GNA CAR ATN NAG AAA 91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
 -5 1 5

NNG AAC AAG ATC AGC AAA RAR TGY CAR NAN GNR NNY GGA GTG TCN 136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
 10 15 20

CAA GAG AYN ATN RNC AAA GYY CGC ANN GGT GNC TNG GNN GAY GAT 181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

CCY AAA NTG AAR NRN CAN GTY YTY TGC NTN NCN ARG ARN RCY GGN 226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
 40 45 50

NTG GCN ACN GAA NCN GGA GAN RYN RNN GTN GAN GTR YTN ARR GNN 271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
 55 60 65

AAG NTG ARG NAN GTN RCY RRC AAC GAC GAA GAR RYN GAN AAR ATC 316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile
 70 75 80

RTN NAN AAG TGC GYN GTC AAG ARR GNY ACN NYN GAR GAR ACG GYN 361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
 85 90 95

TNY RAY ACY TTC AAR NNT RTY NNN RAN ARY AAR CCN RAN TTC TCN 406
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110

CCN RTT GAT TRA NYNNYYNNNA YTNNGNNNRNR NTTYRANAAT AAAGNNNNTN 458
Pro Ile Asp *
 115

TNRTNNNRNA AAAAAAAAAA AAAAAA 484

```

```

(2) INFORMATION FOR SEQ ID NO: 46
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v)
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.2
 (ix) FEATURES
 (D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

MOLECULE TYPE: cDNA to

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
NNNNNNNNNA AAAAAAAAAA AAAAAA
```

## (2) INFORMATION FOR SEQ. ID NO: 48

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE:

## (ix) FEATURES

- (D) OTHER INFORMATION: Genral Consensus of Clones,  
B1, B2 and AFP-3

0997696-060701

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
                   Cys          Leu Ile Ser Leu Ile Leu Leu Val Thr Val  
                                 Thr Leu Val          Ala Ala Thr  
                                 Val                                -5  
                   -15                                -10

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 Tyr          Ile          Glu Ala Asp Leu Glu Leu Leu Arg Gln Thr      Ala  
                   1                                5                  10                  His      Asp

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 Lys          Lys Asn Val          Ala          Glu Asp Ile Leu Thr Arg Ala  
 Ala                  Thr                                Ala Val          Lys  
                                 Ala                                Ser          Asn                  30  
 15                                20                                25

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
       Asn Arg Asp Trp Glu                                Leu          Arg Gln Leu Phe  
       Lys          Glu Glu                                          Met          Ala  
                                 35                                40                  45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
       Val Ala Arg Arg Ala Ile Leu Val Ala Ser          Glu Ile Glu  
       Ile Phe          Ala Leu Glu Ile Ile Asp                  Val Val  
       Leu          Asn          Glu          Phe                  Phe Gln  
                                 50                                55                  60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser \*\*\* Asp Glu  
 Ala Asp Thr Phe Arg Glu          Val Thr Arg Asn Thr Asn Asp Pro  
 Leu          His Ile          Thr          Phe Arg Lys          Ser          Asp Asn  
                   65                                70                  75                  Glu His

Glu Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro  
 Lys Ser Glu Asp Leu Ile Glu          Ala          Thr          Glu Asp      Val  
       Thr                                Asn          Thr          Arg                  Val  
                   80                                85                  90

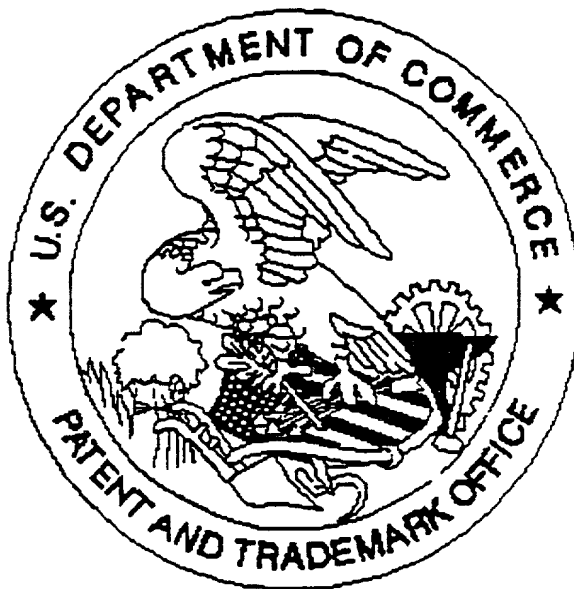
Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro  
 Gln Asp Ser Val Phe Glu Val Thr          Val Val Leu Lys Asn Arg Ser  
       His          Ser Ala Asn Phe                                Met          Asp  
                                                                   His                  Asp  
 95                                100                                105                  110

Asp Phe Ser Pro Ile Asp \*\*\* \*\*\* \*  
 Asn          Phe Gly Asp Leu Phe Val \*  
 Lys                  Val                                \*  
                                 115

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*Drawings*

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